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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=12; day=5; hr=9; min=4; sec=21; ms=55;]

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Reviewer Comments:

<210> 1

<211> 390

<212> PRT

<213> Homo sapien

* * * * *

Please change the spelling of "Homo sapien" to "Homo sapiens."

<210> 16

<211> 20

<212> PRT

<213> synthetic

* * * * *

For SEQ ID # 16, numeric identifier <213> can only be one of three choices, "Scientific name, i.e. Genus/species, Unknown or Artificial Sequence." For all sequences using "Unknown or Artificial sequence", for numeric identifier <213>, a mandatory feature is required to explain the source of the genetic material. The feature consists of <220>, which remains blank, and <223>, which states the source of the genetic material. Suggest using "Artificial sequence" for numeric identifier <213> and "Synthetic" for numeric identifier <223> in the mandatory feature. Please make all necessary changes.

Application No: 10585499 Version No: 1.0

Input Set:

Output Set:

Started: 2008-11-18 12:10:27.981
Finished: 2008-11-18 12:10:29.193
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 212 ms
Total Warnings: 16
Total Errors: 1
No. of SeqIDs Defined: 17
Actual SeqID Count: 17

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
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W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)
E 356	Organism is not permitted in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)

SEQUENCE LISTING

<110> The Government of the United States as represented by the
Secretary, Department of Health and Human Services

<120> COMPOSITIONS AND METHODS FOR THE HIGH EFFICIENCY EXPRESSION OF
THE TRANSFORMING GROWTH FACTOR-BETA SUPERGENE FAMILY

<130> NIHA-0186

<140> 10585499

<141> 2008-11-18

<150> US 60/534,379

<151> 2004-01-06

<160> 17

<170> PatentIn version 3.3

<210> 1

<211> 390

<212> PRT

<213> Homo sapien

<400> 1

Met Pro Pro Ser Gly Leu Arg Leu Leu Leu Leu Leu Leu Pro Leu Leu
1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Thr His Asn Glu Ile Tyr Asp Lys Phe Lys Gln Ser Thr
115 120 125

His Ser Ile Tyr Met Phe Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
165 170 175

Asn Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
195 200 205

Ser Arg Gly Gly Glu Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser
210 215 220

Cys Asp Ser Arg Asp Asn Thr Leu Gln Val Asp Ile Asn Gly Phe Thr
225 230 235 240

Thr Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu Gln
260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser
275 280 285

Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys
290 295 300

Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn
305 310 315 320

Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr
325 330 335

Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala
340 345 350

Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr
355 360 365

Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val
370 375 380

Arg Ser Cys Lys Cys Ser
385 390

<210> 2
<211> 390
<212> PRT
<213> pig

<400> 2

Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
35 40 45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Leu Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
115 120 125

His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu

145		150		155		160									
Lys	Leu	Lys	Val	Glu	Gln	His	Val	Glu	Leu	Tyr	Gln	Lys	Tyr	Ser	Asn
			165						170					175	
Asp	Ser	Trp	Arg	Tyr	Leu	Ser	Asn	Arg	Leu	Leu	Ala	Pro	Ser	Asp	Ser
			180						185					190	
Pro	Glu	Trp	Leu	Ser	Phe	Asp	Val	Thr	Gly	Val	Val	Arg	Gln	Trp	Leu
			195					200					205		
Thr	Arg	Arg	Glu	Ala	Ile	Glu	Gly	Phe	Arg	Leu	Ser	Ala	His	Cys	Ser
			210					215					220		
Cys	Asp	Ser	Lys	Asp	Asn	Thr	Leu	His	Val	Glu	Ile	Asn	Gly	Phe	Asn
225					230					235					240
Ser	Gly	Arg	Arg	Gly	Asp	Leu	Ala	Thr	Ile	His	Gly	Met	Asn	Arg	Pro
				245					250					255	
Phe	Leu	Leu	Leu	Met	Ala	Thr	Pro	Leu	Glu	Arg	Ala	Gln	His	Leu	His
			260						265				270		
Ser	Ser	Arg	His	Arg	Arg	Ala	Leu	Asp	Thr	Asn	Tyr	Cys	Phe	Ser	Ser
			275					280					285		
Thr	Glu	Lys	Asn	Cys	Cys	Val	Arg	Gln	Leu	Tyr	Ile	Asp	Phe	Arg	Lys
			290					295					300		
Asp	Leu	Gly	Trp	Lys	Trp	Ile	His	Glu	Pro	Lys	Gly	Tyr	His	Ala	Asn
305					310					315					320
Phe	Cys	Leu	Gly	Pro	Cys	Pro	Tyr	Ile	Trp	Ser	Leu	Asp	Thr	Gln	Tyr
				325					330					335	
Ser	Lys	Val	Leu	Ala	Leu	Tyr	Asn	Gln	His	Asn	Pro	Gly	Ala	Ser	Ala
			340						345				350		
Ala	Pro	Cys	Cys	Val	Pro	Gln	Ala	Leu	Glu	Pro	Leu	Pro	Ile	Val	Tyr
			355					360					365		
Tyr	Val	Gly	Arg	Lys	Pro	Lys	Val	Glu	Gln	Leu	Ser	Asn	Met	Ile	Val
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Arg Ser Cys Lys Cys Ser
385 390

<210> 3
<211> 414
<212> PRT
<213> Homo sapien

<400> 3

Met His Tyr Cys Val Leu Ser Ala Phe Leu Ile Leu His Leu Val Thr
1 5 10 15

Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp Gln Phe
20 25 30

Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu
35 40 45

Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Glu Glu Val Pro
50 55 60

Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu
65 70 75 80

Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser Asp Glu
85 90 95

Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Pro Phe Phe
100 105 110

Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg
115 120 125

Ile Val Arg Phe Asp Val Ser Ala Met Glu Lys Asn Ala Ser Asn Leu
130 135 140

Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg
145 150 155 160

Val Pro Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp
165 170 175

Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr
180 185 190

Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val His
195 200 205

Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu
210 215 220

His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro
225 230 235 240

Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp Gly Thr
245 250 255

Ser Thr Tyr Thr Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys
260 265 270

Lys Asn Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser
275 280 285

Tyr Arg Leu Glu Ser Gln Gln Thr Asn Arg Arg Lys Lys Arg Ala Leu
290 295 300

Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu Arg
305 310 315 320

Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile His
325 330 335

Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro Tyr
340 345 350

Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu Ser Leu Tyr Asn
355 360 365

Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln Asp
370 375 380

Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Lys Thr Pro Lys Ile
385 390 395 400

Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser

405

410

<210> 4
 <211> 412
 <212> PRT
 <213> Homo sapien

<400> 4

Met Lys Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn
 1 5 10 15

Phe Ala Thr Val Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe
 20 25 30

Gly His Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu
 35 40 45

Ser Lys Leu Arg Leu Thr Ser Pro Pro Glu Pro Thr Val Met Thr His
 50 55 60

Val Pro Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu
 65 70 75 80

Glu Glu Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Asn Thr
 85 90 95

Glu Ser Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln
 100 105 110

Gly Leu Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr
 115 120 125

Ser Lys Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Arg Thr
 130 135 140

Asn Leu Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser
 145 150 155 160

Ser Lys Arg Asn Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro
 165 170 175

Asp Glu His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro
 180 185 190

Thr	Arg	Gly	Thr	Ala	Glu	Trp	Leu	Ser	Phe	Asp	Val	Thr	Asp	Thr	Val			
		195					200						205					
Arg	Glu	Trp	Leu	Leu	Arg	Arg	Glu	Ser	Asn	Leu	Gly	Leu	Glu	Ile	Ser			
	210					215					220							
Ile	His	Cys	Pro	Cys	His	Thr	Phe	Gln	Pro	Asn	Gly	Asp	Ile	Leu	Glu			
225					230					235					240			
Asn	Ile	His	Glu	Val	Met	Glu	Ile	Lys	Phe	Lys	Gly	Val	Asp	Asn	Glu			
			245						250					255				
Asp	Asp	His	Gly	Arg	Gly	Asp	Leu	Gly	Arg	Leu	Lys	Lys	Gln	Lys	Asp			
		260						265					270					
His	His	Asn	Pro	His	Leu	Ile	Leu	Met	Met	Ile	Pro	Pro	His	Arg	Leu			
		275					280					285						
Asp	Asn	Pro	Gly	Gln	Gly	Gly	Gln	Arg	Lys	Lys	Arg	Ala	Leu	Asp	Thr			
	290					295					300							
Asn	Tyr	Cys	Phe	Arg	Asn	Leu	Glu	Glu	Asn	Cys	Cys	Val	Arg	Pro	Leu			
305					310					315					320			
Tyr	Ile	Asp	Phe	Arg	Gln	Asp	Leu	Gly	Trp	Lys	Trp	Val	His	Glu	Pro			
			325						330					335				
Lys	Gly	Tyr	Tyr	Ala	Asn	Phe	Cys	Ser	Gly	Pro	Cys	Pro	Tyr	Leu	Arg			
			340					345					350					
Ser	Ala	Asp	Thr	Thr	His	Ser	Thr	Val	Leu	Gly	Leu	Tyr	Asn	Thr	Leu			
		355					360						365					
Asn	Pro	Glu	Ala	Ser	Ala	Ser	Pro	Cys	Cys	Val	Pro	Gln	Asp	Leu	Glu			
	370					375					380							
Pro	Leu	Thr	Ile	Leu	Tyr	Tyr	Val	Gly	Arg	Thr	Pro	Lys	Val	Glu	Gln			
385					390				395						400			
Leu	Ser	Asn	Met	Val	Val	Lys	Ser	Cys	Lys	Cys	Ser							
			405						410									

<210> 5
<211> 18
<212> PRT
<213> rat

<400> 5

Met Lys Trp Val Thr Phe Leu Leu Leu Leu Phe Ile Ser Gly Ser Ala
1 5 10 15

Phe Ser

<210> 6
<211> 36
<212> DNA
<213> Chinese hamster

<400> 6

gcgataccg ggtataccat ggccacctca gcaagt 36

<210> 7
<211> 33
<212> DNA
<213> Chinese hamster

<400> 7

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<210> 8
<211> 56
<212> DNA
<213> Homo sapien

<400> 8

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<210> 9
<211> 30
<212> DNA
<213> Homo sapien

<400> 9

tagtctcgag ttatcagctg cacttgcagg 30

<210> 10
<211> 45
<212> DNA
<213> rat

<400> 10

aaagggggat cgcaccat gaagtgggta acctttctcc tcctc 45

<210> 11
<211> 45
<212> DNA
<213> rat

<400> 11
agaaaaggca gaaccggaga tgaagaggag gaggagaaag gttac 45

<210> 12
<211> 39
<212> DNA
<213> pig

<400> 12
cgctcagtg ccactgttc ctgtgacagc aaagataac 39

<210> 13
<211> 39
<212> DNA
<213> pig

<400> 13
gttatctttg ctgtcacagg aacagtgggc actgaggcg 39

<210> 14
<211> 33
<212> DNA
<213> pig

<400> 14
ggatccctgt ccacctcaa gaccatcgac atg 33

<210> 15
<211> 33
<212> DNA
<213> pig

<400> 15
catgtcgatg gtcttgagg tggacaggga tcc 33

<210> 16
<211> 20
<212> PRT
<213> synthetic

<400> 16

His His His His His His His His Leu Ser Thr Ser Lys Thr Ile Asp
1 5 10 15

Met Glu Leu Val
20

<210> 17
<211> 20
<212> PRT
<213> pig

<400> 17

Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys
1 5 10 15

Val Arg Gln Leu
20